



## SEQUENCE LISTING

<110> ..Rauch, Charles  
Walczak, Henning

<120> RECEPTOR THAT BINDS TRAIL

<130> 2625-E

<140> US 09/378,045

<141> 1999-08-20

<150> US 08/883,036

<151> 1997-06-26

<150> US 08/869,852

<151> 1997-06-04

<150> US 08/829,536

<151> 1997-03-28

<150> US 08/815,255

<151> 1997-03-12

<150> US 08/799,861

<151> 1997-02-13

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1323

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1323)

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| atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc cgg aaa | 48 |
| Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys |    |
| 1 5 10 15   |    |

|   |    |
|---|----|
| agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc | 96 |
| Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg | 144 |
| Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu |     |
| 35 40 45  |     |

|   |     |
|---|-----|
| gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag | 192 |
| Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg | 240 |
| Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu |     |
| 65 70 75 80   |     |

|   |     |
|---|-----|
| tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc | 288 |
| Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser |     |
| 85 90 95  |     |
| tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc | 336 |
| Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe |     |
| 100 105 110   |     |
| tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg | 384 |
| Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro |     |
| 115 120 125   |     |
| tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc | 432 |
| Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe |     |
| 130 135 140   |     |
| cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt | 480 |
| Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys |     |
| 145 150 155 160   |     |
| ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc | 528 |
| Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile |     |
| 165 170 175   |     |
| gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca | 576 |
| Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro |     |
| 180 185 190   |     |
| gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc | 624 |
| Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro |     |
| 195 200 205   |     |
| tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc | 672 |
| Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val |     |
| 210 215 220   |     |
| ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc | 720 |
| Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val |     |
| 225 230 235 240   |     |
| ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag | 768 |
| Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu |     |
| 245 250 255   |     |
| cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc | 816 |
| Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu |     |
| 260 265 270   |     |
| aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa | 864 |
| Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu |     |
| 275 280 285   |     |
| atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc | 912 |
| Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser |     |
| 290 295 300   |     |
| ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct | 960 |
| Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser |     |
| 305 310 315 320   |     |

|   |      |
|---|------|
| cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag | 1008 |
| Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu |      |
| 325 330 335   |      |
| act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac | 1056 |
| Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp |      |
| 340 345 350   |      |
| tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata | 1104 |
| Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile |      |
| 355 360 365   |      |
| aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg | 1152 |
| Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr |      |
| 370 375 380   |      |
| atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac | 1200 |
| Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His |      |
| 385 390 395 400   |      |
| acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag | 1248 |
| Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln |      |
| 405 410 415   |      |
| aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa | 1296 |
| Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu |      |
| 420 425 430   |      |
| ggg aat gca gac tct gcc atg tcc taa                             | 1323 |
| Gly Asn Ala Asp Ser Ala Met Ser                                 |      |
| 435 440   |      |

<210> 2  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 2

|   |  |
|---|--|
| Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys |  |
| 1 5 10 15   |  |
| Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro |  |
| 20 25 30  |  |
| Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu |  |
| 35 40 45  |  |
| Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln |  |
| 50 55 60  |  |
| Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu |  |
| 65 70 75 80   |  |
| Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser |  |



Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp  
 340 345 350

Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile  
 355 360 365

Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr  
 370 375 380

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His  
 385 390 395 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln  
 405 410 415

Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu  
 420 425 430

Gly Asn Ala Asp Ser Ala Met Ser  
 435 440

<210> 3  
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<220>  
 <221> CDS  
 <222> (3)..(155)

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 <222> (149)..(149)  
 <223> n is a, c, g, or t

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 ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc 47  
 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro  
 1 5 10 15

ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat 95  
 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn  
 20 25 30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg 143  
 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu

35 40 45 157

tnc acn atg ctg at  
 Xaa Thr Met Leu  
 50

<210> 4  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (48)..(48)  
 <223> The 'Xaa' at location 48 stands for Tyr, Cys, Ser, or Phe.

<400> 4

Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe  
 1 5 10 15

Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu  
 20 25 30

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa  
 35 40 45

Thr Met Leu  
 50

<210> 5  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> FLAG peptide

<400> 5

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 6  
 <211> 3159  
 <212> DNA  
 <213> Artificial Sequence

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cgggattgcg gatccgcgat gatatcgttg atcctcgagt gcggccgcag tatgcaaaaa 120

|  |      |
|--|------|
| aaagccccgct cattagggcgg gctcttggca gaacatatcc atcgcggtccg ccatctccag | 180  |
| dagccgcacg cgggcgcacgt cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt   | 240  |
| gctcctgtcg ttgaggaccc ggctaggctg gcgggggttg cttactgggt agcagaatga    | 300  |
| atcaccgata cgcgagcgaa cgtgaagcga ctgctgctgc aaaacgtctg cgacctgagc    | 360  |
| aacaacatga atggtcttcg gtttccgtgt ttcgtaaagt ctggaaacgc ggaagtcagc    | 420  |
| gccctgcacc attatgttcc ggatctgcat cgcaggatgc tgctggctac cctgtggaac    | 480  |
| acctacatct gtattaacga agcgtctggca ttgacctga gtgatttttc tctgggtccc    | 540  |
| ccgcatccat accgccagtt gtttaccctc acaacgttcc agtaaccggg catgttcac     | 600  |
| atcagtaacc cgtatcgtga gcatcctctc tcgtttcatc ggtatcatta ccccatgaa     | 660  |
| cagaaattcc cccttacacg gaggcacaa gtgaccaaac aggaaaaaac cgcccttaac     | 720  |
| atggccccgct ttatcagaag ccagacatta acgcttctgg agaaactcaa cgagctggac   | 780  |
| gcggatgaac aggcagacat ctgtgaatcg cttcacgacc acgctgatga gctttaccgc    | 840  |
| agctgcctcg cgcgtttcgg tgatgacggg gaaaacctct gacacatgca gctcccggag    | 900  |
| acggtcacag cttgtctgta agcggatgcc gggagcagac aagccccgtca gggcgcgtca   | 960  |
| gcgggtgttg gcgggtgtcg gggcgcagcc atgaccagc cacgtagcga tagcggagt      | 1020 |
| tatactgggt taactatgcg gcatcagagc agattgtact gagagtgcac catatgcgg     | 1080 |
| gtgaaatacc gcacagatgc gtaaggagaa aataccgcac caggcgctct tccgcttcct    | 1140 |
| cgtcactga ctcgctgcgc tcggtcgttc ggctgcggcg agcgggtatca gctcactcaa    | 1200 |
| aggcggtaat acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa    | 1260 |
| aaggccagca aaaggccagg aaccgtaaaa aggcgcggtt gctggcggtt tccataggg     | 1320 |
| tccgcccccc tgacgagcat caaaaaatc gacgtcaag tcagaggtgg cgaaaccgca      | 1380 |
| caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc    | 1440 |
| cgacctgcc gcttaccgga tacctgtccg ctttctccc ttcgggaagc gtggcgcttt      | 1500 |
| ctcatagctc acgctgtagg tatctcagtt cgggtgtaggt cgttcgctcc aagctgggct   | 1560 |
| gtgtgcacga accccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg    | 1620 |
| agtccaaccc ggtaagacac gacttatcgc cactggcagc agccaggcgc gccttggcct    | 1680 |
| aagaggccac tggtaacagg attagcagag cgaggatatgt aggcgggtgct acagagttct  | 1740 |
| tgaagtgggt gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc    | 1800 |
| tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg    | 1860 |
| ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc    | 1920 |

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| aagaagatcc  | tttgatcttt  | tctacggggt | ctgacgctca  | gtggaacgaa | aactcacgtt | 1980 |
| aagggatttt  | ggtcattgaga | ttatcaaaaa | ggatcttcac  | ctagatcctt | ttaaattaaa | 2040 |
| aatgaagttt  | taaatcaatc  | taaagtatat | atgagtaaac  | ttggtctgac | agttaccaat | 2100 |
| gcttaatcag  | tgaggcacct  | atctcagcga | tctgtctatt  | tcgttcatcc | atagttgcct | 2160 |
| gactccccgt  | cgtgtagata  | actacgatac | gggaggggctt | accatctggc | cccagtgctg | 2220 |
| caatgatacc  | gcgagacca   | cgctcaccgg | ctccagattt  | atcagcaata | aaccagccag | 2280 |
| ccggaagggc  | cgagcgcaga  | agtggctctg | caactttatc  | cgctccatc  | cagtctatta | 2340 |
| attgttgccg  | ggaagctaga  | gtaagtagtt | cgccagttaa  | tagtttgccg | aacgttggtg | 2400 |
| ccattgctgc  | aggcatcgtg  | gtgtcacgct | cgtcgtttgg  | tatggcttca | ttcagctccg | 2460 |
| gttcccaacg  | atcaaggcga  | gttacatgat | ccccatggtt  | gtgcaaaaaa | gcggttagct | 2520 |
| ccttcgggtc  | tccgatcgtt  | gtcagaagta | agttggccgc  | agtgttatca | ctcatgggta | 2580 |
| tggcagcact  | gcataattct  | cttactgtca | tgccatccgt  | aagatgcttt | tctgtgactg | 2640 |
| gtgagtactc  | aaccaagtca  | ttctgagaat | agtgtatgcg  | gcgaccgagt | tgctcttgcc | 2700 |
| cggcgtcaac  | acgggataat  | accgcgccac | atagcagaac  | tttaaaagtg | ctcatcattg | 2760 |
| gaaaacgttc  | ttcggggcga  | aaactctcaa | ggatcttacc  | gctgttgaga | tccagttcga | 2820 |
| tgtaaccac   | tcgtgcaccc  | aactgatctt | cagcatcttt  | tactttcacc | agcgtttctg | 2880 |
| ggtgagcaaa  | aacaggaagg  | caaatgccc  | caaaaaaggg  | aataagggcg | acacggaaat | 2940 |
| gttgaatact  | catactcttc  | ctttttcaat | attattgaag  | catttatcag | ggttattgtc | 3000 |
| tcattgagcgg | atacatattt  | gaatgtattt | agaaaaataa  | acaaataggg | gttccgcgca | 3060 |
| catttccccg  | aaaagtgcc   | cctgacgtct | aagaaacat   | tattatcatg | acattaacct | 3120 |
| ataaaaatag  | gcgtatcacg  | aggcccttct | gtcttcaag   |            |            | 3159 |